

SEQUENCE LISTING

<110> CNRS

<120> STARCH GRANULES CONTAINING A RECOMBINANT POLYPEPTIDE
OF INTEREST, A METHOD OF OBTAINING THEM AND THEIR USES

<130> WOB 99 AB CNR AMYL

<140> US 09/980,771

<141> 2001-11-15

<150> FR 99/06494

<151> 1999-05-21

<160> 9

<170> PatentIn version 3.1

<210> 1

<211> 3117

<212> DNA

<213> Chlamydomonas reinhardtii

<400> 1

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<210> 2

<211> 2124

<212> DNA

<213> artificial sequence

<220>

<223> fragment of the complete sequence of cDNA coding
for the GBSSI of *Chlamydomonas reinhardtii*

<220>

<221> CDS

<222> (1)..(2124)

<223>

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cgt gag ctt gct cgt ggc tcc gca cgc aag tcc acc tcg cgc tcg gct 144
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Val Thr Gly Ala Thr Gly Ala Thr Cys Ala Leu Asp Ile Val Met Val
50 55 60

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65 70 75 80

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Thr Gly Gly Leu Pro Ile Glu Leu Val Lys Arg Gly His Arg Val Met
85 90 95

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acc att gcc cct cgc tac gac cag tac gct gac gcc tgg gac acc tcg 336
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gct att gag gct gcc cgc gtg ctg ccc ttc ggc ccc ggc gag gac tgc Ala Ile Glu Ala Ala Arg Val Leu Pro Phe Gly Pro Gly Glu Asp Cys 180 185 190	576
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Ala Ala Glu Val Ala Pro Trp Ser Lys Thr Gly Gly Leu Gly Asp Val
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Thr Gly Gly Leu Pro Ile Glu Leu Val Lys Arg Gly His Arg Val Met
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 Lys Val Trp Gly Lys Thr Gly Ser Lys Leu Tyr Gly Pro Arg Ser Gly
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 Lys Asp Glu Tyr Gln Pro Lys Gly Gln Phe Thr Lys Ala Lys Ser Val
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 225 230 235 240
 Phe Lys Asp Thr Lys Leu Pro Gln Ala Ala Phe Asp Lys Leu Ala Phe
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 Ser Asp Gly Tyr Ala Lys Val Tyr Thr Glu Ala Thr Pro Met Glu Glu
 260 265 270
 Asp Glu Lys Pro Pro Leu Thr Gly Lys Thr Tyr Lys Lys Ile Asn Trp
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 465 470 475 480
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 485 490 495
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 for the GBSSI of *Chlamydomonas reinhardtii* and
 coding for the mature GBSSI protein

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 <222> (1)..(1953)
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Gly Leu Val Asp Thr Val Lys Glu Gly Val Thr Gly Phe His Met Gly	
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Gly Val Ala Thr Ala Lys Lys Glu Glu Ile Lys Val Pro Val Ala Glu	
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580 585 590	
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Pro Ala Leu Pro Ala Thr Ala Lys Pro Lys Thr Ala Gly Leu Lys Leu	
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<210> 5
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<223> fragment of the complete sequence of cDNA coding
 for the GBSSI of *Chlamydomonas reinhardtii* and
 coding for the mature GBSSI protein

<400> 5

Ala	Leu	Asp	Ile	Val	Met	Val	Ala	Ala	Glu	Val	Ala	Pro	Trp	Ser	Lys	1	5	10	15
Thr	Gly	Gly	Leu	Gly	Asp	Val	Thr	Gly	Gly	Leu	Pro	Ile	Glu	Leu	Val	20	25	30	
Lys	Arg	Gly	His	Arg	Val	Met	Thr	Ile	Ala	Pro	Arg	Tyr	Asp	Gln	Tyr	35	40	45	
Ala	Asp	Ala	Trp	Asp	Thr	Ser	Val	Val	Val	Asp	Ile	Met	Gly	Glu	Lys	50	55	60	
Val	Arg	Tyr	Phe	His	Ser	Ile	Lys	Lys	Gly	Val	His	Arg	Val	Trp	Ile	65	70	75	80
Asp	His	Pro	Trp	Phe	Leu	Ala	Lys	Val	Trp	Gly	Lys	Thr	Gly	Ser	Lys	85	90	95	
Leu	Tyr	Gly	Pro	Arg	Ser	Gly	Ala	Asp	Tyr	Leu	Asp	Asn	His	Lys	Arg	100	105	110	
Phe	Ala	Leu	Phe	Cys	Lys	Ala	Ala	Ile	Glu	Ala	Ala	Arg	Val	Leu	Pro	115	120	125	
Phe	Gly	Pro	Gly	Glu	Asp	Cys	Val	Phe	Val	Ala	Asn	Asp	Trp	His	Ser	130	135	140	
Ala	Leu	Val	Pro	Val	Leu	Leu	Lys	Asp	Glu	Tyr	Gln	Pro	Lys	Gly	Gln	145	150	155	160
Phe	Thr	Lys	Ala	Lys	Ser	Val	Leu	Ala	Ile	His	Asn	Ile	Ala	Phe	Gln	165	170	175	
Gly	Arg	Met	Trp	Glu	Glu	Ala	Phe	Lys	Asp	Thr	Lys	Leu	Pro	Gln	Ala	180	185	190	
Ala	Phe	Asp	Lys	Leu	Ala	Phe	Ser	Asp	Gly	Tyr	Ala	Lys	Val	Tyr	Thr	195	200	205	
Glu	Ala	Thr	Pro	Met	Glu	Glu	Asp	Glu	Lys	Pro	Pro	Leu	Thr	Gly	Lys	210	215	220	
Thr	Tyr	Lys	Lys	Ile	Asn	Trp	Leu	Lys	Gly	Gly	Ile	Ile	Ala	Ala	Asp	225	230	235	240
Lys	Leu	Val	Thr	Val	Ser	Pro	Asn	Tyr	Ala	Thr	Glu	Ile	Ala	Ala	Asp	245	250	255	
Ala	Ala	Gly	Gly	Val	Glu	Leu	Asp	Thr	Val	Ile	Arg	Ala	Lys	Gly	Ile	260	265	270	

Glu Gly Ile Val Asn Gly Met Asp Ile Glu Glu Trp Asn Pro Lys Thr
 275 280 285
 Asp Lys Phe Leu Ser Ala Pro Tyr Asp Gln Asn Ser Val Tyr Ala Gly
 290 295 300
 Lys Ala Ala Ala Lys Glu Ala Leu Gln Ala Glu Leu Gly Leu Pro Val
 305 310 315 320
 Asp Pro Thr Ala Pro Leu Phe Ala Phe Ile Gly Arg Leu Glu Glu Gln
 325 330 335
 Lys Gly Val Asp Ile Ile Leu Ala Ala Leu Pro Lys Ile Leu Ala Thr
 340 345 350
 Pro Lys Val Gln Ile Ala Ile Leu Gly Thr Gly Lys Ala Ala Tyr Glu
 355 360 365
 Lys Leu Val Asn Ala Ile Gly Thr Lys Tyr Lys Gly Arg Ala Lys Gly
 370 375 380
 Val Val Lys Phe Ser Ala Pro Leu Ala His Met Leu Thr Ala Gly Ala
 385 390 395 400
 Asp Phe Met Leu Val Pro Ser Arg Phe Glu Pro Cys Gly Leu Ile Gln
 405 410 415
 Leu His Ala Met His Tyr Gly Thr Val Pro Val Val Ala Ser Thr Gly
 420 425 430
 Gly Leu Val Asp Thr Val Lys Glu Gly Val Thr Gly Phe His Met Gly
 435 440 445
 Ala Leu Asn Pro Asp Lys Leu Asp Glu Ala Asp Ala Asp Ala Leu Ala
 450 455 460
 Ala Thr Val Arg Arg Ala Ser Glu Val Phe Ala Gly Gly Arg Tyr Pro
 465 470 475 480
 Glu Met Val Ala Asn Cys Ile Ser Gln Asp Leu Ser Trp Ser Lys Pro
 485 490 495
 Ala Gln Lys Trp Glu Gly Leu Leu Glu Glu Val Val Tyr Gly Lys Gly
 500 505 510
 Gly Val Ala Thr Ala Lys Lys Glu Glu Ile Lys Val Pro Val Ala Glu
 515 520 525
 Lys Ile Pro Gly Asp Leu Pro Ala Val Ser Tyr Ala Pro Asn Thr Leu
 530 535 540
 Lys Pro Val Ser Ala Ser Val Glu Gly Asn Gly Ala Ala Ala Pro Lys
 545 550 555 560
 Val Gly Thr Thr Ala Pro Ala Met Gly Ala Trp Arg Ala Thr Thr Pro
 565 570 575
 Ser Gly Pro Ser Pro Ala Ala Ala Thr Pro Lys Val Thr Thr Tyr Lys
 580 585 590

Pro Ala Leu Pro Ala Thr Ala Lys Pro Lys Thr Ala Gly Leu Lys Leu
595 600 605

Ala Gly Glu Ala Ser Thr Thr Ser Thr Ser Glu Asn Gly Ala Ala Ser
610 615 620

Asn Gly Asn Gly Asn Gly Ala Ser Ala Ser Lys Thr Ser Ala Ala Lys
625 630 635 640

Pro Leu Val Ser Ala Ala Thr Arg Lys Ser Ala
645 650

<210> 6

<211> 1314

<212> DNA

<213> artificial sequence

<220>

<223> fragment of the complete cDNA coding for
the GBSSI of *Chlamydomonas reinhardtii*

<220>

<221> CDS

<222> (1)..(1314)

<223>

<400> 6

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Ala Leu Asp Ile Val Met Val Ala Ala Glu Val Ala Pro Trp Ser Lys
1 5 10 15

acg ggc ggc ctg ggc gat gtg act ggt ggc ctg cct att gag ctg gtc 96
Thr Gly Gly Leu Gly Asp Val Thr Gly Gly Leu Pro Ile Glu Leu Val
20 25 30

aag cgc ggc cac cgc gtc atg acc att gcc cct cgc tac gac cag tac 144
Lys Arg Gly His Arg Val Met Thr Ile Ala Pro Arg Tyr Asp Gln Tyr
35 40 45

gct gac gcc tgg gac acc tcg gtg gtc gtg gac atc atg ggc gag aag 192
Ala Asp Ala Trp Asp Thr Ser Val Val Val Asp Ile Met Gly Glu Lys
50 55 60

gtc cgc tac ttc cac tcc atc aag aag ggc gtg cac cgc gtg tgg att 240
Val Arg Tyr Phe His Ser Ile Lys Lys Gly Val His Arg Val Trp Ile
65 70 75 80

gac cac ccc tgg ttc ctg gcc aag gtc tgg ggc aag acc ggc tcc aag 288
Asp His Pro Trp Phe Leu Ala Lys Val Trp Gly Lys Thr Gly Ser Lys
85 90 95

ctg tac ggc ccc cgc tcc ggc gct gac tac ctg gac aac cac aag cgc 336
Leu Tyr Gly Pro Arg Ser Gly Ala Asp Tyr Leu Asp Asn His Lys Arg
100 105 110

ttc gcc ctg ttc tgc aag gcc gct att gag gct gcc cgc gtg ctg ccc 384
Phe Ala Leu Phe Cys Lys Ala Ala Ile Glu Ala Ala Arg Val Leu Pro
115 120 125

ttc ggc ccc ggc gag gac tgc gtc ttc gtg gcc aac gac tgg cac tcc Phe Gly Pro Gly Glu Asp Cys Val Phe Val Ala Asn Asp Trp His Ser 130 135 140	432
gcc ctg gtg ccc gtc ctg ctg aag gac gag tac cag ccc aag ggc cag Ala Leu Val Pro Val Leu Leu Lys Asp Glu Tyr Gln Pro Lys Gly Gln 145 150 155 160	480
ttc acc aag gcc aag tcg gtg ctg gct atc cac aac atc gcc ttc cag Phe Thr Lys Ala Lys Ser Val Leu Ala Ile His Asn Ile Ala Phe Gln 165 170 175	528
ggc cgc atg tgg gag gag gct ttc aag gac acg aag ctg ccc cag gcc Gly Arg Met Trp Glu Glu Ala Phe Lys Asp Thr Lys Leu Pro Gln Ala 180 185 190	576
gcc ttt gac aag ctg gcc ttc tcg gac ggc tat gcc aag gtt tac act Ala Phe Asp Lys Leu Ala Phe Ser Asp Gly Tyr Ala Lys Val Tyr Thr 195 200 205	624
gag gcc acc ccc atg gag gag gac gag aag ccc ccg ctg acg gga aag Glu Ala Thr Pro Met Glu Glu Asp Glu Lys Pro Pro Leu Thr Gly Lys 210 215 220	672
acc tac aag aag atc aac tgg ctg aag ggt ggc att atc gcc gcc gac Thr Tyr Lys Lys Ile Asn Trp Leu Lys Gly Gly Ile Ile Ala Ala Asp 225 230 235 240	720
aag ctg gtg act gtg tcg ccc aac tac gcg acc gag atc gct gcc gat Lys Leu Val Thr Val Ser Pro Asn Tyr Ala Thr Glu Ile Ala Ala Asp 245 250 255	768
gcc gcc ggc ggt gtg gag ctg gac acc gtc atc cgc gcc aag ggc att Ala Ala Gly Gly Val Glu Leu Asp Thr Val Ile Arg Ala Lys Gly Ile 260 265 270	816
gag ggc att gtg aac ggc atg gac att gag gag tgg aac ccc aag acc Glu Gly Ile Val Asn Gly Met Asp Ile Glu Glu Trp Asn Pro Lys Thr 275 280 285	864
gac aag ttc ctg tct gcg ccc tac gac cag aac agc gtc tac gcc ggc Asp Lys Phe Leu Ser Ala Pro Tyr Asp Gln Asn Ser Val Tyr Ala Gly 290 295 300	912
aag gcc gcc gcc aag gag gcc ctg cag gcc gag ctg ggc ctg cct gtg Lys Ala Ala Ala Lys Glu Ala Leu Gln Ala Glu Leu Gly Leu Pro Val 305 310 315 320	960
gac ccc acc gcc ccc ctg ttc gcc ttc atc ggc cgc ctg gag gag cag Asp Pro Thr Ala Pro Leu Phe Ala Phe Ile Gly Arg Leu Glu Glu Gln 325 330 335	1008
aag ggt gtg gac atc atc ctg gcc gcc ctg ccc aag atc ctg gcc acc Lys Gly Val Asp Ile Ile Leu Ala Ala Leu Pro Lys Ile Leu Ala Thr 340 345 350	1056
ccc aag gtg cag atc gcc atc ctg ggt acc ggc aag gcc gcc tac gag Pro Lys Val Gln Ile Ala Ile Leu Gly Thr Gly Lys Ala Ala Tyr Glu 355 360 365	1104

aag ctg gtg aac gcc atc ggc acc aag tac aag ggc cgc gcc aag ggc 1152
 Lys Leu Val Asn Ala Ile Gly Thr Lys Tyr Lys Gly Arg Ala Lys Gly
 370 375 380

gtg gtc aag ttc tcg gcg ccc ctg gcg cac atg ctc acc gcc ggc gcc 1200
 Val Val Lys Phe Ser Ala Pro Leu Ala His Met Leu Thr Ala Gly Ala
 385 390 395 400

gac ttc atg ctg gtg ccc tcg cgc ttc gag ccc tgc ggc ctg atc cag 1248
 Asp Phe Met Leu Val Pro Ser Arg Phe Glu Pro Cys Gly Leu Ile Gln
 405 410 415

ctg cac gcc atg cac tac ggt acc gtg ccc gtg gta gcc tcc acc ggc 1296
 Leu His Ala Met His Tyr Gly Thr Val Pro Val Val Ala Ser Thr Gly
 420 425 430

ggc ctg gtc gac acc gtc 1314
 Gly Leu Val Asp Thr Val
 435

<210> 7
 <211> 438
 <212> PRT
 <213> artificial sequence

<220>
 <223> fragment of the complete cDNA coding
 for the GBSSI of *Chlamydomonas reinhardtii*

<400> 7
 Ala Leu Asp Ile Val Met Val Ala Ala Glu Val Ala Pro Trp Ser Lys
 1 5 10 15
 Thr Gly Gly Leu Gly Asp Val Thr Gly Gly Leu Pro Ile Glu Leu Val
 20 25 30
 Lys Arg Gly His Arg Val Met Thr Ile Ala Pro Arg Tyr Asp Gln Tyr
 35 40 45
 Ala Asp Ala Trp Asp Thr Ser Val Val Val Asp Ile Met Gly Glu Lys
 50 55 60
 Val Arg Tyr Phe His Ser Ile Lys Lys Gly Val His Arg Val Trp Ile
 65 70 75 80
 Asp His Pro Trp Phe Leu Ala Lys Val Trp Gly Lys Thr Gly Ser Lys
 85 90 95
 Leu Tyr Gly Pro Arg Ser Gly Ala Asp Tyr Leu Asp Asn His Lys Arg
 100 105 110
 Phe Ala Leu Phe Cys Lys Ala Ala Ile Glu Ala Ala Arg Val Leu Pro
 115 120 125
 Phe Gly Pro Gly Glu Asp Cys Val Phe Val Ala Asn Asp Trp His Ser
 130 135 140
 Ala Leu Val Pro Val Leu Leu Lys Asp Glu Tyr Gln Pro Lys Gly Gln
 145 150 155 160

Phe Thr Lys Ala Lys Ser Val Leu Ala Ile His Asn Ile Ala Phe Gln
 165 170 175
 Gly Arg Met Trp Glu Glu Ala Phe Lys Asp Thr Lys Leu Pro Gln Ala
 180 185 190
 Ala Phe Asp Lys Leu Ala Phe Ser Asp Gly Tyr Ala Lys Val Tyr Thr
 195 200 205
 Glu Ala Thr Pro Met Glu Glu Asp Glu Lys Pro Pro Leu Thr Gly Lys
 210 215 220
 Thr Tyr Lys Lys Ile Asn Trp Leu Lys Gly Gly Ile Ile Ala Ala Asp
 225 230 235 240
 Lys Leu Val Thr Val Ser Pro Asn Tyr Ala Thr Glu Ile Ala Ala Asp
 245 250 255
 Ala Ala Gly Gly Val Glu Leu Asp Thr Val Ile Arg Ala Lys Gly Ile
 260 265 270
 Glu Gly Ile Val Asn Gly Met Asp Ile Glu Glu Trp Asn Pro Lys Thr
 275 280 285
 Asp Lys Phe Leu Ser Ala Pro Tyr Asp Gln Asn Ser Val Tyr Ala Gly
 290 295 300
 Lys Ala Ala Ala Lys Glu Ala Leu Gln Ala Glu Leu Gly Leu Pro Val
 305 310 315 320
 Asp Pro Thr Ala Pro Leu Phe Ala Phe Ile Gly Arg Leu Glu Glu Gln
 325 330 335
 Lys Gly Val Asp Ile Ile Leu Ala Ala Leu Pro Lys Ile Leu Ala Thr
 340 345 350
 Pro Lys Val Gln Ile Ala Ile Leu Gly Thr Gly Lys Ala Ala Tyr Glu
 355 360 365
 Lys Leu Val Asn Ala Ile Gly Thr Lys Tyr Lys Gly Arg Ala Lys Gly
 370 375 380
 Val Val Lys Phe Ser Ala Pro Leu Ala His Met Leu Thr Ala Gly Ala
 385 390 395 400
 Asp Phe Met Leu Val Pro Ser Arg Phe Glu Pro Cys Gly Leu Ile Gln
 405 410 415
 Leu His Ala Met His Tyr Gly Thr Val Pro Val Val Ala Ser Thr Gly
 420 425 430
 Gly Leu Val Asp Thr Val
 435

<210> 8

<211> 1593

<212> DNA

<213> artificial sequence

<220>
 <223> fragment of the complete cDNA coding for
 the GBSSI of *Chlamydomonas reinhardtii*

<220>
 <221> CDS
 <222> (1)..(1593)
 <223>

<400> 8
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 Ala Leu Asp Ile Val Met Val Ala Ala Glu Val Ala Pro Trp Ser Lys
 1 5 10 15
 acg ggc ggc ctg ggc gat gtg act ggt ggc ctg cct att gag ctg gtc 96
 Thr Gly Gly Leu Gly Asp Val Thr Gly Gly Leu Pro Ile Glu Leu Val
 20 25 30
 aag cgc ggc cac cgc gtc atg acc att gcc cct cgc tac gac cag tac 144
 Lys Arg Gly His Arg Val Met Thr Ile Ala Pro Arg Tyr Asp Gln Tyr
 35 40 45
 gct gac gcc tgg gac acc tcg gtg gtc gtg gac atc atg ggc gag aag 192
 Ala Asp Ala Trp Asp Thr Ser Val Val Val Asp Ile Met Gly Glu Lys
 50 55 60
 gtc cgc tac ttc cac tcc atc aag aag ggc gtg cac cgc gtg tgg att 240
 Val Arg Tyr Phe His Ser Ile Lys Lys Gly Val His Arg Val Trp Ile
 65 70 75 80
 gac cac ccc tgg ttc ctg gcc aag gtc tgg ggc aag acc ggc tcc aag 288
 Asp His Pro Trp Phe Leu Ala Lys Val Trp Gly Lys Thr Gly Ser Lys
 85 90 95
 ctg tac ggc ccc cgc tcc ggc gct gac tac ctg gac aac cac aag cgc 336
 Leu Tyr Gly Pro Arg Ser Gly Ala Asp Tyr Leu Asp Asn His Lys Arg
 100 105 110
 ttc gcc ctg ttc tgc aag gcc gct att gag gct gcc cgc gtg ctg ccc 384
 Phe Ala Leu Phe Cys Lys Ala Ala Ile Glu Ala Ala Arg Val Leu Pro
 115 120 125
 ttc ggc ccc ggc gag gac tgc gtc ttc gtg gcc aac gac tgg cac tcc 432
 Phe Gly Pro Gly Glu Asp Cys Val Phe Val Ala Asn Asp Trp His Ser
 130 135 140
 gcc ctg gtg ccc gtc ctg ctg aag gac gag tac cag ccc aag ggc cag 480
 Ala Leu Val Pro Val Leu Leu Lys Asp Glu Tyr Gln Pro Lys Gly Gln
 145 150 155 160
 ttc acc aag gcc aag tcg gtg ctg gct atc cac aac atc gcc ttc cag 528
 Phe Thr Lys Ala Lys Ser Val Leu Ala Ile His Asn Ile Ala Phe Gln
 165 170 175
 ggc cgc atg tgg gag gag gct ttc aag gac acg aag ctg ccc cag gcc 576
 Gly Arg Met Trp Glu Glu Ala Phe Lys Asp Thr Lys Leu Pro Gln Ala
 180 185 190
 gcc ttt gac aag ctg gcc ttc tcg gac ggc tat gcc aag gtt tac act 624
 Ala Phe Asp Lys Leu Ala Phe Ser Asp Gly Tyr Ala Lys Val Tyr Thr
 195 200 205

gag gcc acc ccc atg gag gag gac gag aag ccc ccg ctg acg gga aag Glu Ala Thr Pro Met Glu Glu Asp Glu Lys Pro Pro Leu Thr Gly Lys 210 215 220	672
acc tac aag aag atc aac tgg ctg aag ggt ggc att atc gcc gcc gac Thr Tyr Lys Lys Ile Asn Trp Leu Lys Gly Gly Ile Ile Ala Ala Asp 225 230 235 240	720
aag ctg gtg act gtg tcg ccc aac tac gcg acc gag atc gct gcc gat Lys Leu Val Thr Val Ser Pro Asn Tyr Ala Thr Glu Ile Ala Ala Asp 245 250 255	768
gcc gcc ggc ggt gtg gag ctg gac acc gtc atc cgc gcc aag ggc att Ala Ala Gly Gly Val Glu Leu Asp Thr Val Ile Arg Ala Lys Gly Ile 260 265 270	816
gag ggc att gtg aac ggc atg gac att gag gag tgg aac ccc aag acc Glu Gly Ile Val Asn Gly Met Asp Ile Glu Glu Trp Asn Pro Lys Thr 275 280 285	864
gac aag ttc ctg tct gcg ccc tac gac cag aac agc gtc tac gcc ggc Asp Lys Phe Leu Ser Ala Pro Tyr Asp Gln Asn Ser Val Tyr Ala Gly 290 295 300	912
aag gcc gcc gcc aag gag gcc ctg cag gcc gag ctg ggc ctg cct gtg Lys Ala Ala Ala Lys Glu Ala Leu Gln Ala Glu Leu Gly Leu Pro Val 305 310 315 320	960
gac ccc acc gcc ccc ctg ttc gcc ttc atc ggc cgc ctg gag gag cag Asp Pro Thr Ala Pro Leu Phe Ala Phe Ile Gly Arg Leu Glu Glu Gln 325 330 335	1008
aag ggt gtg gac atc atc ctg gcc gcc ctg ccc aag atc ctg gcc acc Lys Gly Val Asp Ile Ile Leu Ala Ala Leu Pro Lys Ile Leu Ala Thr 340 345 350	1056
ccc aag gtg cag atc gcc atc ctg ggt acc ggc aag gcc gcc tac gag Pro Lys Val Gln Ile Ala Ile Leu Gly Thr Gly Lys Ala Ala Tyr Glu 355 360 365	1104
aag ctg gtg aac gcc atc ggc acc aag tac aag ggc cgc gcc aag ggc Lys Leu Val Asn Ala Ile Gly Thr Lys Tyr Lys Gly Arg Ala Lys Gly 370 375 380	1152
gtg gtc aag ttc tcg gcg ccc ctg gcg cac atg ctc acc gcc ggc gcc Val Val Lys Phe Ser Ala Pro Leu Ala His Met Leu Thr Ala Gly Ala 385 390 395 400	1200
gac ttc atg ctg gtg ccc tcg cgc ttc gag ccc tgc ggc ctg atc cag Asp Phe Met Leu Val Pro Ser Arg Phe Glu Pro Cys Gly Leu Ile Gln 405 410 415	1248
ctg cac gcc atg cac tac ggt acc gtg ccc gtg gta gcc tcc acc ggc Leu His Ala Met His Tyr Gly Thr Val Pro Val Val Ala Ser Thr Gly 420 425 430	1296
ggc ctg gtc gac acc gtc aag gag ggc gtc acc ggc ttc cac atg ggc Gly Leu Val Asp Thr Val Lys Glu Gly Val Thr Gly Phe His Met Gly 435 440 445	1344

gcc ctg aac ccc gac aag ctg gac gag gct gac gcc gac gcc ctg gcc 1392
 Ala Leu Asn Pro Asp Lys Leu Asp Glu Ala Asp Ala Asp Ala Leu Ala
 450 455 460

gcc acc gtg cgc cgt gcc agc gag gtg ttt gcg ggc ggc cgc tac ccc 1440
 Ala Thr Val Arg Arg Ala Ser Glu Val Phe Ala Gly Gly Arg Tyr Pro
 465 470 475 480

gag atg gtg gcc aac tgc atc agc cag gac ctg tcc tgg tcc aag ccc 1488
 Glu Met Val Ala Asn Cys Ile Ser Gln Asp Leu Ser Trp Ser Lys Pro
 485 490 495

gcc cag aag tgg gag ggc ctg ctg gag gag gtg gtg tac ggc aag ggc 1536
 Ala Gln Lys Trp Glu Gly Leu Leu Glu Glu Val Val Tyr Gly Lys Gly
 500 505 510

ggc gtg gcc acc gcc aag aag gag gag atc aag gtg ccc gtt gcc gag 1584
 Gly Val Ala Thr Ala Lys Lys Glu Glu Ile Lys Val Pro Val Ala Glu
 515 520 525

aag atc ccc 1593
 Lys Ile Pro
 530

<210> 9
 <211> 531
 <212> PRT
 <213> artificial sequence

<220>
 <223> fragment of the complete cDNA coding for
 the GBSSI of *Chlamydomonas reinhardtii*

<400> 9
 Ala Leu Asp Ile Val Met Val Ala Ala Glu Val Ala Pro Trp Ser Lys
 1 5 10 15

Thr Gly Gly Leu Gly Asp Val Thr Gly Gly Leu Pro Ile Glu Leu Val
 20 25 30

Lys Arg Gly His Arg Val Met Thr Ile Ala Pro Arg Tyr Asp Gln Tyr
 35 40 45

Ala Asp Ala Trp Asp Thr Ser Val Val Val Asp Ile Met Gly Glu Lys
 50 55 60

Val Arg Tyr Phe His Ser Ile Lys Lys Gly Val His Arg Val Trp Ile
 65 70 75 80

Asp His Pro Trp Phe Leu Ala Lys Val Trp Gly Lys Thr Gly Ser Lys
 85 90 95

Leu Tyr Gly Pro Arg Ser Gly Ala Asp Tyr Leu Asp Asn His Lys Arg
 100 105 110

Phe Ala Leu Phe Cys Lys Ala Ala Ile Glu Ala Ala Arg Val Leu Pro
 115 120 125

Phe Gly Pro Gly Glu Asp Cys Val Phe Val Ala Asn Asp Trp His Ser
 130 135 140

Ala	Leu	Val	Pro	Val	Leu	Leu	Lys	Asp	Glu	Tyr	Gln	Pro	Lys	Gly	Gln	
145					150					155					160	
Phe	Thr	Lys	Ala	Lys	Ser	Val	Leu	Ala	Ile	His	Asn	Ile	Ala	Phe	Gln	
				165					170					175		
Gly	Arg	Met	Trp	Glu	Glu	Ala	Phe	Lys	Asp	Thr	Lys	Leu	Pro	Gln	Ala	
			180					185					190			
Ala	Phe	Asp	Lys	Leu	Ala	Phe	Ser	Asp	Gly	Tyr	Ala	Lys	Val	Tyr	Thr	
		195					200					205				
Glu	Ala	Thr	Pro	Met	Glu	Glu	Asp	Glu	Lys	Pro	Pro	Leu	Thr	Gly	Lys	
	210					215					220					
Thr	Tyr	Lys	Lys	Ile	Asn	Trp	Leu	Lys	Gly	Gly	Ile	Ile	Ala	Ala	Asp	
225				230						235					240	
Lys	Leu	Val	Thr	Val	Ser	Pro	Asn	Tyr	Ala	Thr	Glu	Ile	Ala	Ala	Asp	
				245					250					255		
Ala	Ala	Gly	Gly	Val	Glu	Leu	Asp	Thr	Val	Ile	Arg	Ala	Lys	Gly	Ile	
			260					265					270			
Glu	Gly	Ile	Val	Asn	Gly	Met	Asp	Ile	Glu	Glu	Trp	Asn	Pro	Lys	Thr	
	275						280					285				
Asp	Lys	Phe	Leu	Ser	Ala	Pro	Tyr	Asp	Gln	Asn	Ser	Val	Tyr	Ala	Gly	
	290					295					300					
Lys	Ala	Ala	Ala	Lys	Glu	Ala	Leu	Gln	Ala	Glu	Leu	Gly	Leu	Pro	Val	
305					310					315					320	
Asp	Pro	Thr	Ala	Pro	Leu	Phe	Ala	Phe	Ile	Gly	Arg	Leu	Glu	Glu	Gln	
				325					330					335		
Lys	Gly	Val	Asp	Ile	Ile	Leu	Ala	Ala	Leu	Pro	Lys	Ile	Leu	Ala	Thr	
			340					345					350			
Pro	Lys	Val	Gln	Ile	Ala	Ile	Leu	Gly	Thr	Gly	Lys	Ala	Ala	Tyr	Glu	
		355					360					365				
Lys	Leu	Val	Asn	Ala	Ile	Gly	Thr	Lys	Tyr	Lys	Gly	Arg	Ala	Lys	Gly	
	370					375					380					
Val	Val	Lys	Phe	Ser	Ala	Pro	Leu	Ala	His	Met	Leu	Thr	Ala	Gly	Ala	
385					390					395					400	
Asp	Phe	Met	Leu	Val	Pro	Ser	Arg	Phe	Glu	Pro	Cys	Gly	Leu	Ile	Gln	
				405					410					415		
Leu	His	Ala	Met	His	Tyr	Gly	Thr	Val	Pro	Val	Val	Ala	Ser	Thr	Gly	
			420					425					430			
Gly	Leu	Val	Asp	Thr	Val	Lys	Glu	Gly	Val	Thr	Gly	Phe	His	Met	Gly	
		435					440					445				
Ala	Leu	Asn	Pro	Asp	Lys	Leu	Asp	Glu	Ala	Asp	Ala	Asp	Ala	Leu	Ala	
	450					455					460					

Ala Thr Val Arg Arg Ala Ser Glu Val Phe Ala Gly Gly Arg Tyr Pro
465 470 475 480

Glu Met Val Ala Asn Cys Ile Ser Gln Asp Leu Ser Trp Ser Lys Pro
485 490 495

Ala Gln Lys Trp Glu Gly Leu Leu Glu Glu Val Val Tyr Gly Lys Gly
500 505 510

Gly Val Ala Thr Ala Lys Lys Glu Glu Ile Lys Val Pro Val Ala Glu
515 520 525

Lys Ile Pro
530